[P-04]

Crystallization and preliminary X-ray crystallographic studies of Tpa1p from *Saccharomyces cerevisiae*

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The yeast Tpa1 (*T*ermination and *P*oly*A*denylation) protein contains a prolyl and lysyl hydroxylase domain. Tpa1p is ubiquitously distributed throughout the eukaryotic kingdom, from *C. elegans* to humans. Recently, it was proposed that Tpa1 is part of a messenger ribonucleoprotein (mRNP) complex at the 3'-UTR of mRNAs, associates specifically with components of the translation termination complex, and is involved in both translation termination and regulation of normal mRNA decay through translation termination-coupled poly(A) shortening. To gain insight into the Tpa1 function at the molecular level,we have overexpressed and crystallized Tpa1p. X-ray diffraction data were collected to 2.5 Å using synchrotron X-rays. The native crystal belong to the monoclinic space group C2, with unit cell parameters of a = 236 Å, b = 136 Å, c = 83 Å, and β = 90.0. The asymmetric unit contains three monomers, giving a crystal volume per protein mass (Vm) of 3.0 $Å^3$ Da^{-1} and a solvent content of 59%. Single wavelength anomalous diffraction data were collected at 100 K from a crystal of the SeMet-substituted protein. Model building is in progress.